



Sequence Listing

<110> APROGEN INC.
<120> HUMANIZED ANTIBODY AND PROCESS FOR PREPARING SAME
<130> PCA30215/APG
<140> US/10/508,759
<141> 2004-09-22
<150> KR10-2002-0015708
<151> 2002-03-22
<160> 38
<170> KopatentIn 1.71
<210> 1
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain HZVII

<400> 1
caggtccagc tgggtgcagtc tggagctgaa gtgaagaagc ctggggcctc agtgaaggtt 60
tcctgcaaag cttctggcta caccttcacc agtgcttgga tgaactgggt gcgacaggcc 120
cctggacagg gtcttgagt gatgggacgg atttatccta gtggtggaag cactagctac 180
gcacagaagt tccagggcag agtcacaatg actgcagaca aatccacgag cacagtctac 240
atggagctca gcagcctgag atctgaggac acggcggtgt attactgtgc aagagagtac 300
cgggttgccc gttggggcca aggaactctg gtcactgtct ctca 345

<210> 2
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain HZVII

<400> 2
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Ala Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ala
20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Tyr Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Arg Val Ala Arg Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 3
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain HZIV

<400> 3
gatatcgtga tgacccaaac tccactttct ttgtcgggta cccctggaca accagcctct 60
atctcttgca agtcaagtca ggcctctta tatagtaatg gaaaaaccta tttgaattgg 120
ttattacaga agccaggcca gcctccacag cgcctaattct atctgggtgtc taatcggggac 180
tctggagtcc ctgacagggt cagtggcagt ggatcaggaa cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttgaggtt tattactgcg tgcaaggtag acattttcct 300
cagacgttcg gtggaggcac caaggtggaa atcaaa 336

<210> 4
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain HZIV

<400> 4
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30
Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro
35 40 45
Pro Gln Arg Leu Ile Tyr Leu Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly
85 90 95
Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu94

<400> 5
gagaattcac attcacgatg tacttg 26

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR43-1

<400> 6
ctgctgcagc tggacctgac tctggacacc att 33

<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR44-1

<400> 7
caggtccagc tgcagcagtc tggacctgaa ctg 33

<210> 8
<211> 33
<212> DNA
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<220>
<223> oligomer HUR45-1

<400> 8
tgggcccttg gtggaggctg cagagacagt gac 33

<210> 9
<211> 33
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<220>
<223> oligomer HUR46-1

<400> 9
gcctccacca agggcccatc ggtcttcccc ctg 33

<210> 10
<211> 28
<212> DNA
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<220>
<223> oligomer HUR31

<400> 10
cagcggccgc tcatttaccg ggggacag

28

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu86

<400> 11
caaagcttgg aagcaagatg gattca

26

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR48

<400> 12
caagatatcc ccacaggtac cagatac

27

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR49

<400> 13
tgtggggata tcttgatgac ccaaact

27

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR50

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cacagatctt ttgatttcca gcttggt

27

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	atcaaaagat ctgtggctgc accatct	27
<210>	16	
<211>	58	
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<223>	oligomer CK1D	
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<210>	17	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	oligomer YM001N	
<400>	17	
	ccggaattca cattcacgat gtacttg	27
<210>	18	
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<223>	oligomer YM003	
<400>	18	
	tgccccaga ggtgct	16
<210>	19	
<211>	33	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	oligomer ym257	
<400>	19	
	acgcattcag tgcttcttgg atgaactggg tga	33

<210>	20	
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<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	oligomer YM258	
<400>	20	
atccaagaag cactgaatgc gtagccagaa g		31
<210>	21	
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<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	oligomer YM004	
<400>	21	
ccaattcaaa gcggtttttc cattactata taagaggc		38
<210>	22	
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<212>	DNA	
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<223>	oligomer YM009	
<400>	22	
gcagccaccg tacgtttgat ttccaccttg gt		32
<210>	23	
<211>	39	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	oligomer Ryu 166	
<400>	23	
ggatttgtct gcagtcattg tggctctgcc ctggaactt		39
<210>	24	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
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<223>	oligomer Hur 37	
<400>	24	
gacaaatcca cgagcacagt ctacatg		27

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu 118

<400> 25
ctgtggaggc tggcctggct tctgtaataa cca 33

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu 119

<400> 26
ggccagcctc cacagctcct aatctatctg 30

<210> 27
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> variable region of humanized heavy chain KR127VH

<400> 27
caggtccagc tgcagcagtc tggacctgaa ctggtgaagc ctggggcctc agtgaagatt 60
tcctgcaaag cttctggcta cgcattcagt agttcttgga tgaactgggt gaagcagagg 120
cctggacagg gtcttgagtg gattggacgg atttatcctg gagatggaga tactaactac 180
aatgggaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240
atgcagctca gcagcctgac ctctgtggac tctgcggtct atttctgtgc aagagagtac 300
gacgaggctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 28
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> variable region of humanized heavy chain KR127VH

<400> 28
Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Glu Tyr Asp Glu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 Val Ser Ala
 115

<210> 29
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variable region of humanized light chain KR127VK

<400> 29	
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atctcttgca agtcaagtca ggcctctta tatagtaatg gaaaaaccta tttgaattgg	120
ttattacaga ggccaggcca gtctccaaag cgcctaattct atctgggtgtc taaactggac	180
tctggagtcc ctgacagggt cactggcagt ggatcaggaa cagattttac actgaaaatc	240
atcagagtgg aggctgagga tttgggagtt tattactgcg tgcaaggtag acattttcct	300
cagacgttcg gtggaggcac caagctggaa atcaaa	336

<210> 30
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable region of humanized light chain KR127VK

<400> 30
 Asp Ile Leu Met Thr Gln Thr Pro Leu Ile Leu Ser Val Thr Ile Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
 20 25 30
 Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65		70		75		80									
Ile	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Tyr	Cys	Val	Gln	Gly
			85					90						95	
Thr	His	Phe	Pro	Gln	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
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<210> 31
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variable region of humanized heavy chain DP7

<400>	31	
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gtgaagaagc	ctggggcctc	agtgaagggt
		60
tcttgcaagg	catctggata	caccttcacc
agctactata	tgcactgggt	gcgacaggcc
		120
cctggacaag	ggcttgagtg	gatgggaata
atcaacccta	gtggtggtag	cacaagctac
		180
gcacagaagt	tccagggcag	agtcaccatg
accagggaca	cgccacgag	cacagtctac
		240
atggagctga	gcagcctgag	atctgaggac
acggccgtgt	attactgtgc	gaga
		294

<210> 32
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variable region of humanized heavy chain DP7

<400>	32														
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
		20					25					30			
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35				40						45			
Gly	Ile	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Gln	Lys	Phe
	50					55				60					
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr
	65				70				75						80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90						95	
Ala	Arg														

<210> 33

<211> 302
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain DPK12

<400> 33
gatattgtga tgaccagac tccactctct ctgtccgtca cccctggaca gccggcctcc 60
atctcctgca agtctagtca gagcctcctg catagtgatg gaaagaccta tttgtattgg 120
tacctgcaga agccaggcca gcctccacag ctctgatct atgaagtttc caaccggttc 180
tctggagtgc cagatagggt cagtggcagc gggtcaggga cagatttcac actgaaaatc 240
agccgggtgg aggctgagga tgttgggggtt tattactgca tgcaaagtat acagcttcct 300
cc 302

<210> 34
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain DPK12

<400> 34
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30
Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45
Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95
Ile Gln Leu Pro
100

<210> 35
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized heavy chain HZI

<400> 35
caggtccagc tgggtcagtc tggagctgaa gtggtgaagc ctggggcctc agtgaaggtt 60

tcctgcaaag cttctggcta cgcattcagt agttcttggg tgaactgggt gcgacaggcc	120
cctggacagg gtcttgagtg gattggacgg atttatcctg gagatggaga tactaactac	180
gcacagaagt tccagggcaa ggccacactg actgcagaca aatccacgag cacagcctac	240
atggagctca gcagcctgag atctgaggac acggcgggtct atttctgtgc aagagagtac	300
gacgaggctt actggggcca aggaactctg gtcactgtct ctca	345

<210> 36
 <211> 115
 <212> PRT
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<220>
 <223> variable region of humanized heavy chain HZI

<400> 36
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
 20 25 30
 Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Tyr Pro Gly Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Glu Tyr Asp Glu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 Val Ser Ser
 115

<210> 37
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> variable region of humanized light chain HZI

<400> 37	
gatattcttga tgacccaaac tccactttct ttgtcgggta cccctggaca accagcctct	60
atctcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg	120
ttattacaga agccaggcca gtctccaaag cgcctaattct atctggtgtc taaactggac	180
tctggagtcc ctgacagggt cagtggcagt ggatcaggaa cagattttac actgaaaatc	240
agcagagtgg aggctgagga tgttggagtt tattactgcg tgcaagggtac acattttcct	300

cagacgttcg gtggaggcac caaggtggaa atcaaa

336

<210> 38
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain HZI

<400> 38
Asp Ile Leu Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30
Asn Gly Lys Thr Tyr Leu Tyr Trp Leu Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly
85 90 95
Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110